

Result No.	Score	Query Match	Length	DB	ID	Description
1	1362	100.0	1362	9	AF034633	AF034633 Homo sapi
2	857	62.9	1744	9	AC088744	AC088744 Homo sapi
3	508.6	37.3	1295	9	AC079773	AC079773 Homo sapi
4	491.6	36.5	1890	6	AX136281	AX136281 Sequence
5	285	20.9	1797	10	AB041649	AB041649 Mus muscu
6	236.6	17.4	587	6	AX136698	AX136698 Sequence
7	154.2	12.1	1254	22	E11480	E11480 cDNA encodi
8	164.8	12.1	4131	9	HSN1094	X70070 H. sapiens m
9	158.6	11.6	444	6	AL150120	AL150120 Sequence
10	150.4	11.0	110000	2	AL357872_0	AL357872 Homo sapi
11	150.4	11.0	114642	9	AL357033	AL357033 Human DNA
12	133.8	9.8	3917	10	AB017027	AB017027 Mus muscu
13	124.8	9.2	1239	9	AK026195	AK026195 Homo sapi
14	123.2	9.0	170695	2	AL351318	AL351318 Homo sapi
15	123.2	9.0	189476	2	AL157394	AL157394 Homo sapi
16	97.6	7.2	1569	9	HSNTR2REC	Y10148 H. sapiens m
17	96.2	7.1	1676	5	AF082210	AF082210 Homo sapi
18	95.8	7.0	1342	6	E29334	E29334 Novel human
19	89.4	6.6	729	6	AX139107	AX139107 Sequence
20	89.4	6.6	801	6	AX147772	AX147772 Sequence
21	89.4	6.6	1239	9	AF242874	AF242874 Homo sapi
22	89.4	6.6	1248	9	AB041228	AB041228 Homo sapi
23	89.4	6.6	1248	9	AF232402	AF232402 Homo sapi
24	89.4	6.6	1248	9	AF272363	AF272363 Homo sapi
25	89.4	6.6	1594	6	AX109242	AX109242 Sequence
26	89.4	6.6	1594	6	AX109244	AX109244 Sequence
27	89.4	6.6	1658	6	AX109234	AX109234 Sequence
28	89.4	6.6	1658	6	AX109236	AX109236 Sequence
29	89.4	6.6	1658	6	AX109238	AX109238 Sequence
30	89.4	6.6	1658	6	AX109240	AX109240 Sequence
31	89.4	6.6	215088	2	AC008571	AC008571 Homo sapi
32	86.4	6.3	1554	10	MM051908	U51908 Mus musculus
33	85.4	6.3	1529	10	RNNTR2REC	X97121 R. norvegicus
34	83.6	6.1	6787	9	AF363786	AF363786 Homo sapi
35	83.6	6.1	145593	9	AC069523	AC069523 Homo sapi
36	82	6.0	870	9	HSU60181	U60181 Human growth
37	82	6.0	1088	6	AR156353	AR156353 Sequence
38	82	6.0	1101	6	AX156354	AX156354 Sequence
39	82	6.0	1101	9	HSU60179	U60179 Human growth
40	82	6.0	1122	6	AR156354	AR156354 Sequence
41	80.4	5.9	145272	2	AC016938	AC016938 Homo sapi
42	78.6	5.8	836	6	AR156355	AR156355 Sequence
43	77.2	5.7	1092	6	AR156357	AR156357 Sequence
44	77.2	5.7	1350	10	AB001982	AB001982 Rattus norvegicus
45	77.2	5.7	3129	6	AR156356	AR156356 Sequence

ALIGNMENTS

RESULT	1	Score	Match	Length	DB	ID	Description
AF034633							
LOCUS	AF034633	1362 bp	mRNA				
DEFINITION	Homo sapiens						
ACCESSION							
VERSION	AF034633.1	GI:2654160					
KEYWORDS							
SOURCE							
ORGANISM	Homo sapiens						
BELONGS TO							
MATERIALS							
DEFINITION							
COMMENT							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
MEDLINE							

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE	2 (bases 1 to 1362)
AUTHORS	McKee, K.K., Tan, C.P., Palyha, O.C., Liu, J., Feighner, S.D., Hreniuk, D.L., Smith, R.G., Van Der Ploeg, L.H.T. and Howard, A.D.
JOURNAL	Submitted (17-NOV-1997) Biochemistry and Physiology, Merck and Co., Inc., PO Box 2000, Rahway, NJ 07065, USA
FEATURES	location/qualifiers
source	1. 1362
organism	"Homo sapiens"
taxon	9606
chromosome	"21"
map	"2q21-22"
dev_stade	"fetal"
tissue_type	"brain"
gene	1. 1362
GRPR39	1. 1362
GRPR39	/gene="GRPR39"
GRPR39	/product="GRPR39"
GRPR39	/protein_id="AAC26082.1"
GRPR39	/db_xref="GI:2654161"
GRPR39	/translation="MASPILPGSDCSQIDDHSHWPEFEVATWIKITLILWLLIFVAG
GRPR39	LIGNSATIRITVQVQKRGILQKEVTDHMSLACSDILFLIGMFERFISIINPLPTS
GRPR39	SYTUSCKLILFHLFACSYTITLHLTSRPEVIAICHPPRYKAVSGPCQVKLIGFW
GRPR39	VFOSIFGAEWVWVLLWLSVAKWQNMWQYLMQSQKGSLAIGGTRPQLRSSESRV
GRPR39	ARROTIFLKLIVTFLAVWMPNUJRRMMAKPHDWSRVERAYMLLPSETFFY
GRPR39	LSSTINPLIYTVSQQFRYFVOLCRLRSLNHRERLRYHAHST"DSARVORPL
GRPR39	LEFASRQSSARTEKIFLSTFQEAERFQSSKSQSLSLEPNSGAKPANSAAENGFOE
GRPR39	HEV"
BASE COUNT	263
ORIGIN	a 435 c 362 g 302 t
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Best Local Similarity	100.0%; Pred. No. 4.8e-262;
Matches	1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 atgggttcacccaggctccggggagtggccatccatgttgcacatcatatc
Db	1 ATGGCCTCACCCAGCCTCCGGGCAGTGCATGCTGCCAAATCATGTGCACTGATC
QY	61 ccggatgtggggccatctgtatccatccatgttgcgttatactgtatccatc
Db	61 CCCGATGTGGGGCCACTGATCAAATGCCCTTATGGGTACCGATGTC
QY	121 ttctgtatggcccttcggggacacggccaccattccgtggccatgggtgtc
Db	121 TTCTGATGSGCCCTCTGGGAACAGCGCCACCATTCGGTACCCAGGTGCAAG
QY	181 aasqgatacttgtcagaaggggatcacaacatggatgggttgtctgtggatc
Db	181 AAAGGATACTTGCAAGAGGGTGACAGACACACATGGTGGTGGACATC
QY	241 ttgggtttccacggcatggccatctcgatccatctgtggatccatgg
Db	241 TTGGTGTCTCATGGCAGGCCATGTCATGATCATCGATCATCGA
QY	301 acgtccagatcacccgttcgtcaagtcacactttcttcggggctgcgtac
Db	301 ACGTCACACTACACCCGTCCTCAAGCTGCACACTTCTTCAGGCCAGTC
QY	361 gtcacgtctgtcgacgtctgtggactcaatcgatctgggtgttcaccc
Db	361 GCTACGCGCTGCACTGCTGACTGACTGCTTGGGCTACATGCCATCTGACCC
QY	421 ttcaaggttcaagggtgtcgggaccatggccgttgcgggtggatcgatc
Db	421 TTCAAGGTTCAGGAGGTGTCTGAGGCTACTAGGCCACTCAGGCGAAACCAGC
QY	421 TTAGGGTACAGGAGGTGTCTGACAGTCAGTGGTTCAGGATGAGTTGA
Db	421 TTAGGGTACAGGAGGTGTCTGACAGTCAGTGGTTCAGGATGAGTTGA
RESULT	2
AC068744	AC068744 17494 bp DNA
LOCUS	AC068744 17494 bp DNA
DEFINITION	Homo sapiens chromosome 2 clone RP1-666P13 map 2, WORKING DRAFT
SEQUENCE	Homo sapiens chromosome 2, 22 unordered pieces.
ACCESSION	AC068744
VERSION	AC068744.2 GI:10567984
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
Fukuhara: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	

Db	1531	TGATCCCTCCCTCCCTCTGGAGACTTTCATCTAGCTGGTCACTAACCGCGCTC	1472
Qy	1028	tgtacacacgggtctcgaggacttcgtcgagggtctcgagggtctcgccgc	1087
Db	1471	TGTACACGGCTGCTCGCGCAGHTTCGGGGGTTGCTGCGAGGTCG	1412
Qy	1088	tgtcgctcagcggccaaacaaaggaaaggccatcgccatcgccactccaccacg	1147
Db	1411	TGRCGCTCAGCAGCCAAACAGAGAGAGGCGCTGCGTACATGCCAATCCACACG	1352
Qy	1148	acagcgccgtttgtcgaggacccgttgcttcagcqgagccggccactgtcaag	1207
Db	1351	ACACGCCGCCGCTTGTGCGAGCCGGTCTCTCGCGCCTCCCGCGCCAGTCTCTCGAA	1292
Qy	1208	-gagaactcgagaatttcttaagccatttcagcqgagccggccactgtcaag	1266
Db	1291	GGGAGAACTGTAGAGATTTCTTAAGACTTTCAGACCTTTCAGAGCAGGCCAGTCTAAG	1232
Qy	1267	tcccaagtatgtggctcgaggactcgaggccaaactcgaggccgaaaccaccaatct	1326
Db	1231	TCCAGCAGTGTAGCTCGAGTCACTAGGCCAACTCAGGCCGAACACAGCCAATCT	1172
Qy	1327	gctcgaggaaatgttttcaggaggatcgaaatgttgc	1362
Db	1171	GCAGCAGGAAATGTTTCAGGCCATGAGTGTGA	1136
RESULT	5		
AB041649	AB041649	1797 bp mRNA	30-JUN-2000
LOCUS	AB041649	1797 bp mRNA	30-JUN-2000
DEFINITION	Mus musculus brain cDNA, clone MNCB-0671.		
ACCESSION	AB041649		
VERSION	AB041649.1		
KEYWORDS	GI:7670499		
SOURCE			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
REFERENCE	1 (sites)		
AUTHORS	Osada, N., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Sugano, S. and Hashimoto, K.		
TITLE	Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method		
JOURNAL	Unpublished (2000)		
REFERENCE	2 (bases 1 to 1797)		
AUTHORS	Hashimoto, K., Osada, N., Kusuda, J. and Sugano, S.		
JOURNAL	Submitted (13-APR-2000) to the DDBJ/EMBL/GenBank databases.		
COMMENT			
LIB NAME:	sugano mouse brain mnccb		
LAB HOST:	Top10		
VECTOR:	PME18S-FRL3		
1st strand cDNA was primed with an oligo(dT) primer [ATGGCGCTTTCCTTTCCTT] and double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments < 1.5 kb. The SfiI digested PCR product was cloned into distinct Brain sites of PME18S-FRL3. XbaI sites just outside the Brain sites can be used to isolate the cDNA insert. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing (5' end primer [CTCTGCGCTAAAGCTCG], 3' end primer [GAGCTCAGCTCGCGCA]). A part of this sequence is reported in AU035640.			
FEATURES	Location/qualifiers		
source	1. 1797 /organism="Mus musculus"		

QY	646	cgctggaccgtgttcccaagtccacatccggcccttcgtgttctacttcgtggcc
Db	712	CAGGTCAACACCTTCATGTCCTCATATTCCCATGGTGTCACTCGGTCTGAAAC
QY	706	ctctccatagccttcatgtgtgtggaaatcatgtatggcagggtctatggaaaggcagaag
Db	772	ATCATGCCAACAACTGCTGACCCCTCAGGTACCCAGCGGCCAGGGCAAGTGT
QY	766	tcgtctggccggggcacggggctccggcggcgtggaaatggagatccggagagcggaaatggaa
Db	832	ACGGCTGGGGG-----AGCACAGCAATCAGATGCCATCGACCCAGG
QY	826	accggcaggaggagaccatcatccgttcaatggatgtgtgtggatggatggcggtt
Db	886	CGAGGCCCTGGCACGGSgtGGGGTCTACGGCAGGtGTCATCGCCTTGGGTT
QY	886	tagatggcccaaccaggatggaggatcatgggtgtggccaaaccggcactgt
Db	946	TGGCTGCCCTAACACGTGGGCCCTCATCTCTGCTACATCGGATGAGCAGTGG
QY	946	aggctactttccggggctatctgtatccatccatccatccatccatccatccat
Db	1006	CCGGTCCCTCTATGACTTCACACTACTCTACATGGGACCAACGCCACTCTTA
QY	1006	agctcggttcaaccggccctgtacccgggtgtctccgtggagatccgggggtt
Db	1065	AGCTCCACCATCAACCCCATCTGTACAACTCTCTCTGCCAACACTCCGCCACAT
QY	1066	gtggagggtgtgtgtgtggccgtgtcgatgtggcggccaaaccggagaaatggcggcc
Db	1126	CTGGCCACACTGGCTCTGCGGCTGCGGAGGGAGGGAGGG
QY	117	

VERSION AL357872.15 GI:11414584
 KEYWORDS HTG: HTGS_PHASE1.
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Primates; Catarhini; Homidae; Homo.
 1 (bases 1 to 367980)
 Plumb, B.
 TITLE Direct Submission
 JOURNAL Submitted (08-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
 requests: clonequery@sanger.ac.uk On Nov 28, 2000 this sequence version replaced gi:11340280.
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 Center Project name: ba3089
 Center Project Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 346090 bases at least Q40
 Consensus quality: 350708 bases at least Q30
 Insert Size: 362500; sum-of-contigs
 Insert size: 174142; 7.0% error; agarose-fp
 Quality coverage: 4.17x in 020 bases; agarose-fp
 Coverage: 9.44x in 020 bases; agarose-fp
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 55 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 1 3371: contig of 3371 bp in length
 * 3372 3471: gap of 100 bp
 * 3472 6278: contig of 2807 bp in length
 * 6279 6378: gap of 100 bp
 * 6379 11841: contig of 5463 bp in length
 * 11842 11941: gap of 100 bp
 * 11942 17529: contig of 5588 bp in length
 * 17530 17629: gap of 100 bp
 * 17630 25354: contig of 7625 bp in length
 * 25255 30177: contig of 4823 bp in length
 * 30178 30277: gap of 100 bp
 * 30278 33210: contig of 2933 bp in length
 * 33211 33310: gap of 100 bp
 * 33311 43615: contig of 10305 bp in length
 * 43616 43715: gap of 100 bp
 * 43716 47706: contig of 3991 bp in length
 * 47707 47806: gap of 100 bp
 * 47807 51335: contig of 3529 bp in length
 * 51336 51435: gap of 100 bp
 * 51436 53350: contig of 2155 bp in length
 * 53391 53690: gap of 100 bp
 * 53691 56178: contig of 2488 bp in length
 * 56179 56278: gap of 100 bp
 * 56279 59233: contig of 2945 bp in length
 * 59224 59323: gap of 100 bp
 * 59224 63358: contig of 4275 bp in length
 * 63359 63698: gap of 100 bp
 * 63699 77580: contig of 13882 bp in length
 * 77581 77680: gap of 100 bp
 * 77681 81130: contig of 3350 bp in length
 * 81131 81130: gap of 100 bp
 * 81131 90501: contig of 9371 bp in length

90502 90601: gap of 100 bp
 * 90602 98709: contig of 8108 bp in length
 * 98710 98803: gap of 100 bp
 * 98810 107616: contig of 100 bp
 * 107617 107716: gap of 100 bp
 * 107717 114867: contig of 7151 bp in length
 * 114868 114967: gap of 100 bp
 * 114968 123825: contig of 8858 bp in length
 * 123826 123925: gap of 100 bp
 * 123926 126983: contig of 3058 bp in length
 * 126984 127083: gap of 100 bp
 * 127084 130970: contig of 3887 bp in length
 * 130971 131070: gap of 100 bp
 * 131071 136942: contig of 5872 bp in length
 * 136943 137042: gap of 100 bp
 * 137043 144404: contig of 7362 bp in length
 * 144405 144504: gap of 100 bp
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 * 177984 178033: gap of 100 bp
 * 178084 181525: contig of 3442 bp in length
 * 181526 181625: gap of 100 bp
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 * 195092 195191: gap of 100 bp
 * 195192 196115: contig of 2924 bp in length
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 * 206598 206691: gap of 100 bp
 * 206698 220397: contig of 13700 bp in length
 * 220398 220497: gap of 100 bp
 * 220498 222979: contig of 2482 bp in length
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 * 223080 225370: contig of 2291 bp in length
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 * 225471 229357: contig of 3887 bp in length
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 * 229458 231791: contig of 2334 bp in length
 * 231792 231891: gap of 100 bp
 * 231892 235072: contig of 3181 bp in length
 * 235073 235172: gap of 100 bp
 * 235173 241381: contig of 6209 bp in length
 * 241382 241481: gap of 100 bp
 * 241482 250412: contig of 16931 bp in length
 * 250413 258512: gap of 100 bp
 * 258513 267906: contig of 9394 bp in length
 * 267907 268006: gap of 100 bp
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 * 293423 292233: gap of 100 bp
 * 292234 298279: contig of 5756 bp in length
 * 298280 298379: gap of 100 bp
 * 298380 301682: contig of 3303 bp in length
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 * 301783 305013: contig of 3231 bp in length
 * 305014 305113: gap of 100 bp
 * 305114 308387: contig of 3274 bp in length
 * 308388 308487: gap of 100 bp
 * 308488 311059: contig of 2572 bp in length
 * 311060 311159: gap of 100 bp
 * 311160 313655: contig of 2496 bp in length
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 * 313756 316142: contig of 2387 bp in length
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Query Match 11.0%; Score 150.4; DB 2; Length 110000;
 Best Local Similarity 57.1%; Pred. No. 1.4e-20;
 Matches 274; Conservative 0; Mismatches 206; Index 0; Gaps 0;

Q ||| 106 gttgtactgtatcttcgtggatggctttggggacgcgcacccattccggtacc 165
 Db 31063 GGTGACTCTGGCTCTGCGGTGACGGTACGGGTACGCTG 31122

QY 166 cagggtctgtcagaaggatcttgcagaagggttgcacacatgttgatgttq 225
 Db 31123 GCGCGGAGAAGTCTGTCAGAGCAGCGTGCATTACCAACGGGCCCTG 31182

QY 226 gttgtctgtcagaatcttgggttccatctcgatgtccatgttacagatcatc 285
 Db 31183 GGCCTGTCGACGTCACCTGCTGCTGCTGACCTGACATC 31242

QY 286 tggaaatccctcgccgtccaaatccatgttcgttcgtccaaatccatgttcc 345
 Db 31243 TGGGTGACCAACCCCTGGCCCTGCGGACGCCCTACTACTTCGGC 31302

QY 346 gagggcgtcgccgtctgtcgtccaaatccatgttccgtccaaatccatgttcc 405
 Db 31303 GGGCGCTGACCTACCCACGGCCCTAACCTGGCCAGCCCTGAGCTG 31362

QY 406 gccatctgtcacccttcaggatcacaaggctgtgtccggacatggggatgt 465
 Db 31363 GGCATCTGCCACCCCTCAAGGCCAGACCTCATGCCAGAGGCCATCAAGAGTC 31422

QY 466 attggcttcgtctgggtcacccctcgccctgtggcaactgccttgcgtttccatgggt 525

FEATURES source 1. . 367980
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 /db_xref="taxon:9606"
 /clone="RP1-308P9"
 /chromosome="9"
 /clone_1ib="RPCI-11.2"
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 /fragment_chain:1"
 3472. . 6278
 /note="assembly fragment:03347
 /fragment_chain:1"
 6379. . 11841
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 11942. . 17529
 /note="assembly fragment:02196
 /fragment_chain:1"
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 /note="assembly fragment:04994
 /fragment_chain:1"
 2535. . 30177
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 30218. . 33210
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 /fragment_chain:1"
 3311. . 43615
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 43716. . 47706
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 /db_xref="taxon:9606"
 /clone="RP1-93B14"
 /chromosome="20"
 /clone_1ib="RPCI-11.1"
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 /note="Single clone region"
 1. . 285
 /note="match: GSS: EmA0312036"

RESULT 11
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 LOCUS Human DNA sequence from clone RP11-93B14 on chromosome 20 Contains
 DEFINITION the SC21A12 gene for solute carrier family 21 (organic anion
 transporter) member 12, the 5' end of the NTSR1 gene encoding the
 high affinity neurotensin receptor 1, a novel gene, 4 CPG islands,
 BSTS-, STSS and GSSE, complete sequence.
 Db 31483 GACAGAACCGGAGCGACGCCACACGCCGCGCTGGTGTGACCCACATC 31542

ACCESSION AL57033
 VERSION AL57033.19 GI:10443441
 KEYWORDS NTNG; CPG island; neurotensin receptor; NTSR1; organic anion
 transporter; SLC21A12; solute carrier.
 SOURCE Human
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Buterilia; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 114642)
 AUTHORS Heath,P.
 TITLE Direct Submission
 JOURNAL
 COMMENT
 REQUESTS submitted (07-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone
 On Oct 1, 2000 this sequence version replaced gi:10277960.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate Primary accession
 numbers given in the feature table with their source databases:
 Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMEP; Information
 on the WORMEP database can be found at
 http://www.sanger.ac.uk/projects/C-elegans/wormep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 20, constructed by the Sanger Centre Chromosome 20
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Ch20
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-93B14. It may be shorter because we sequence overlapping
 sections only once, for a 100 base overlap. The
 true left end of clone RP11-93B14 is at 1 in this sequence. The
 true left end of clone RP5-88517 is at 11453 in this sequence.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. RP11-93B14 is from
 the library RPCI-11.1 constructed by the group of Pieter de Jong.
 For further details see
 http://www.sanger.ac.uk/bacpac/home.htm
 VECTOR: pBAC3.6
 LOCATION/QUALIFIERS

